Center for
Computational
Biology (CCB)

Learning Based Approaches for Brain Anatomical Structure Parsing/Segmentation

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Joint work with

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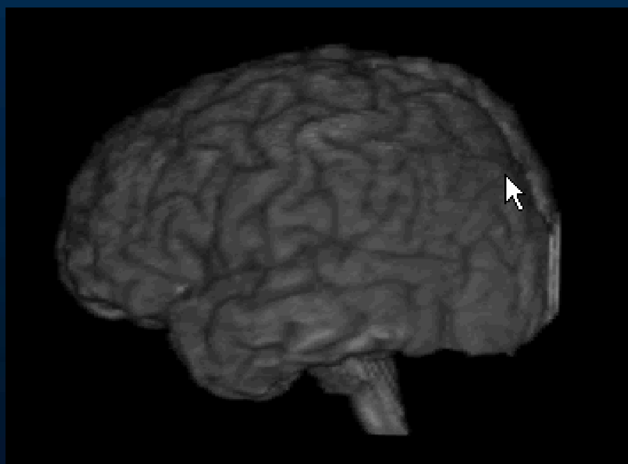
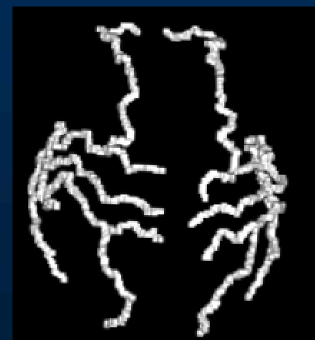
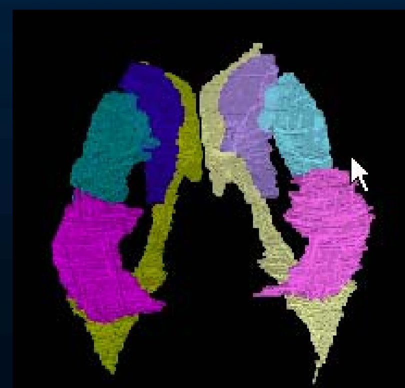
Brain Anatomical Structure Parsing

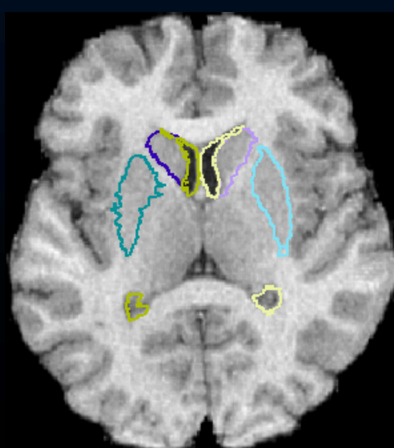


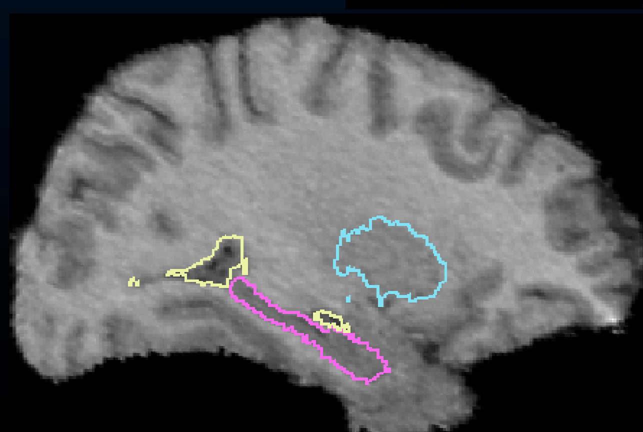


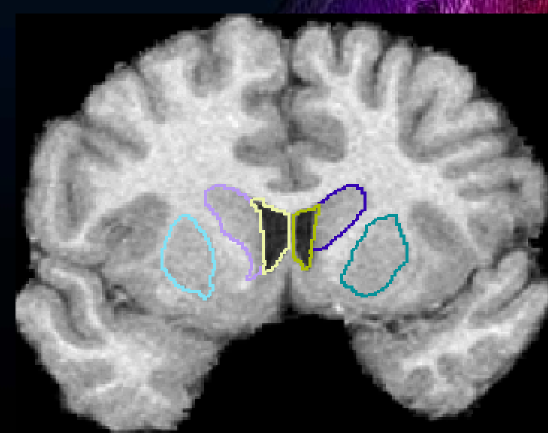
Some cortical structures:
major sulci curves



Some sub-cortical
structures

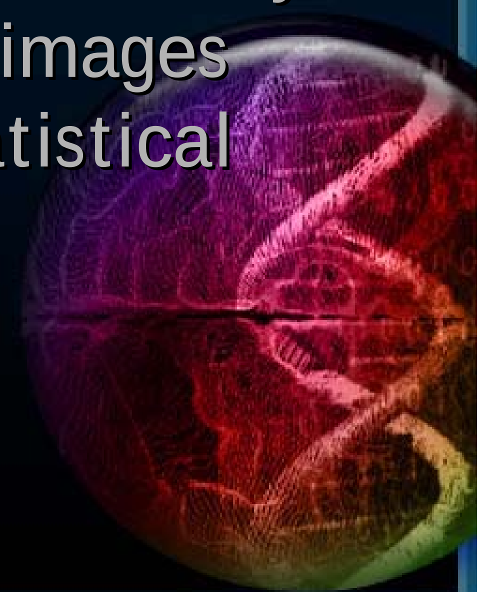




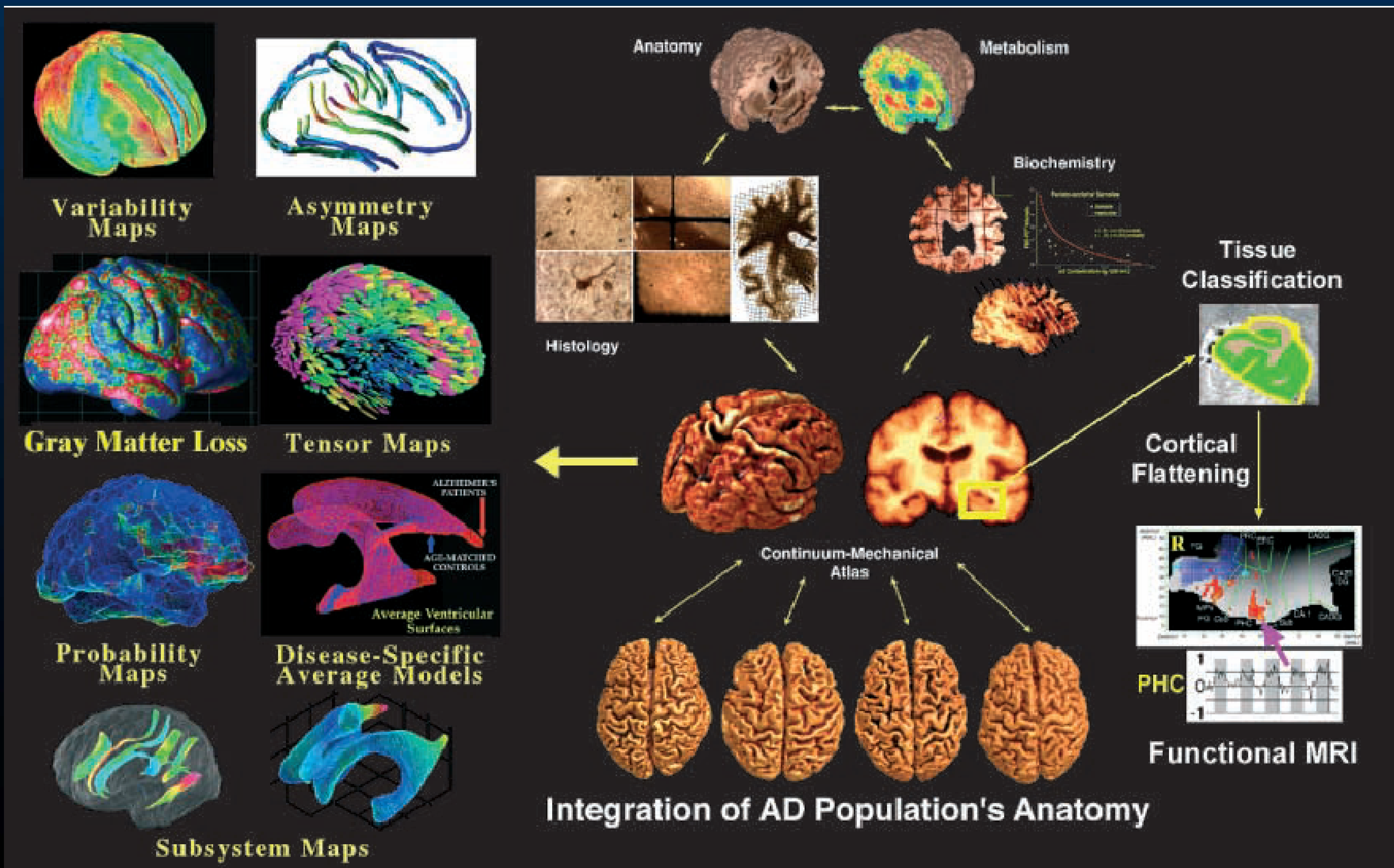


Why is the task important?

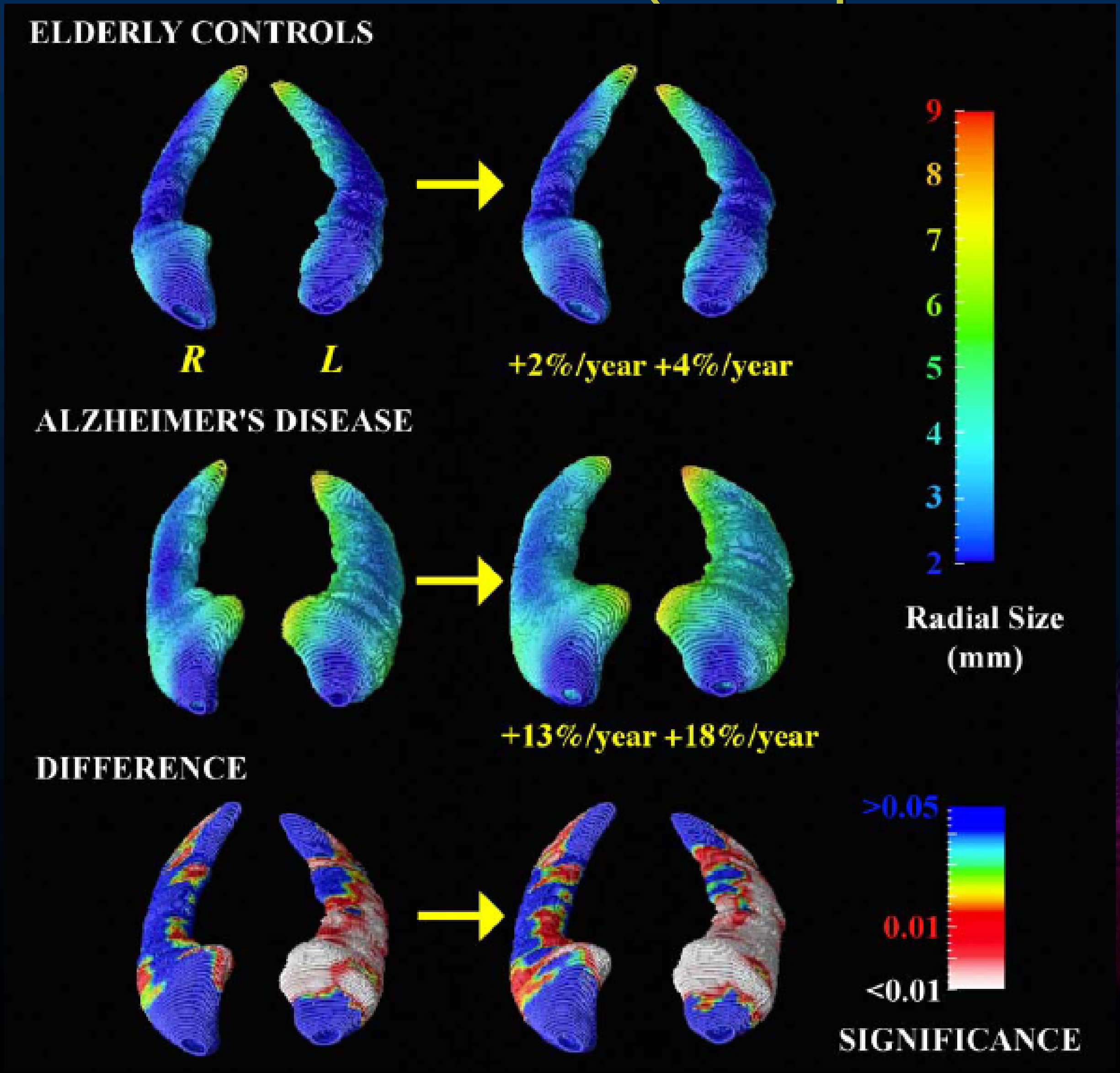
- Sub-cortical and cortical structures are of great anatomical and clinical importance.
- Their shapes provide viable information about brain growth and various diseases.
- We can use these anatomical structures as key landmarks to register different brain images for us to study the brain atlas and statistical properties.



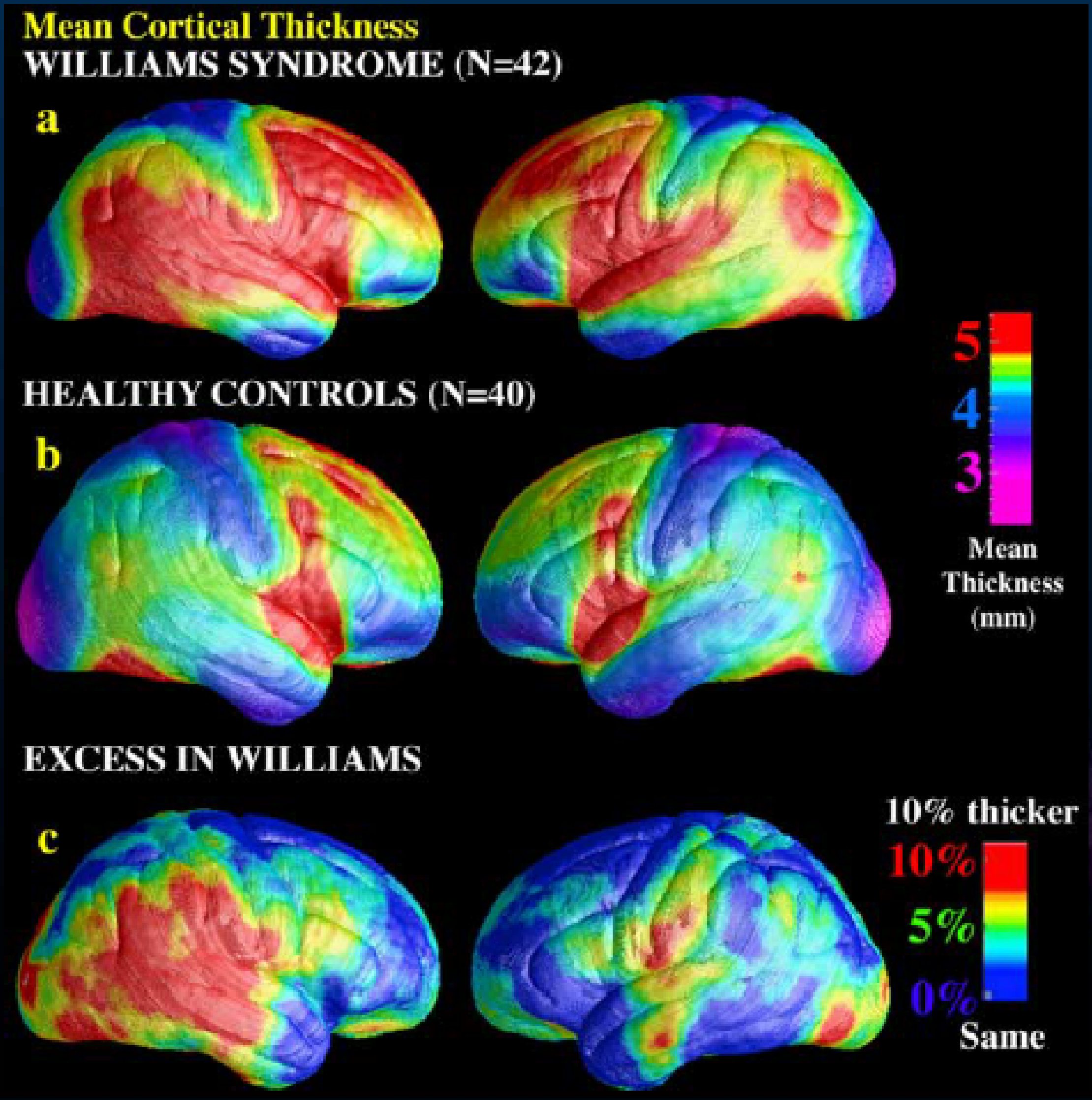
Element of a disease-specific atlas (Thompson and Toga 2004)



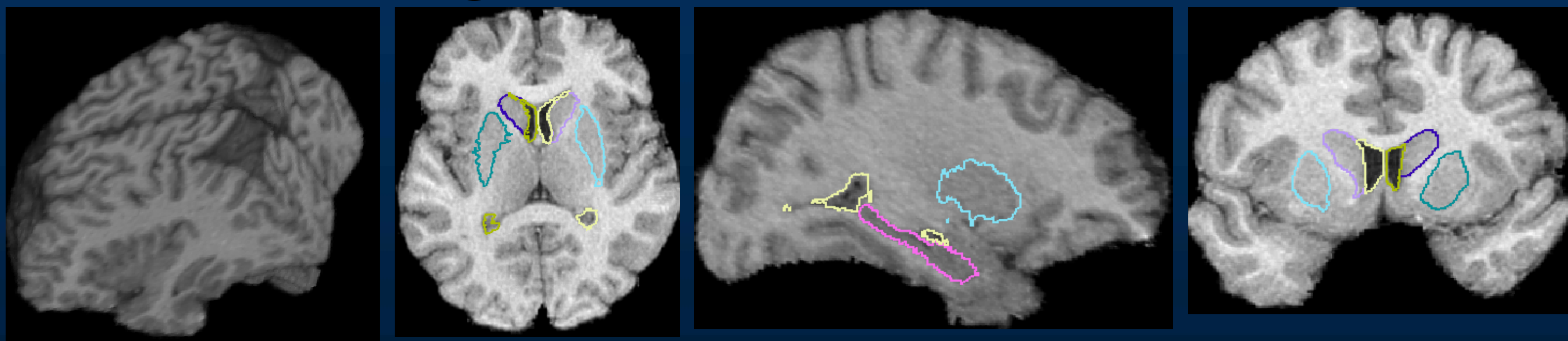
Mapping hippocampal change in Alzheimer disease (Thompson et al. 2004)



Cortical thickness mapping in Williams Syndrome (Thompson et al. 2005)

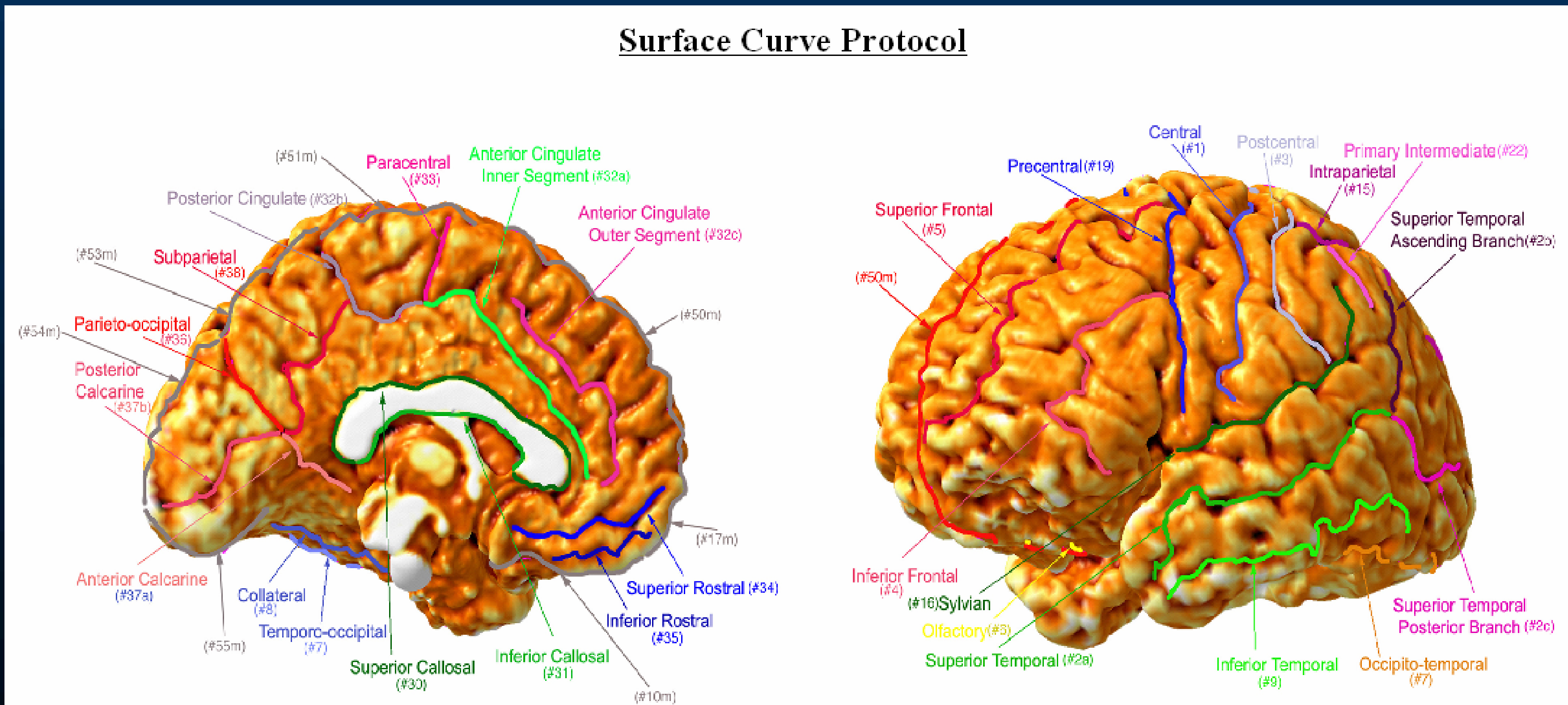


Challenges for Manual Annotation

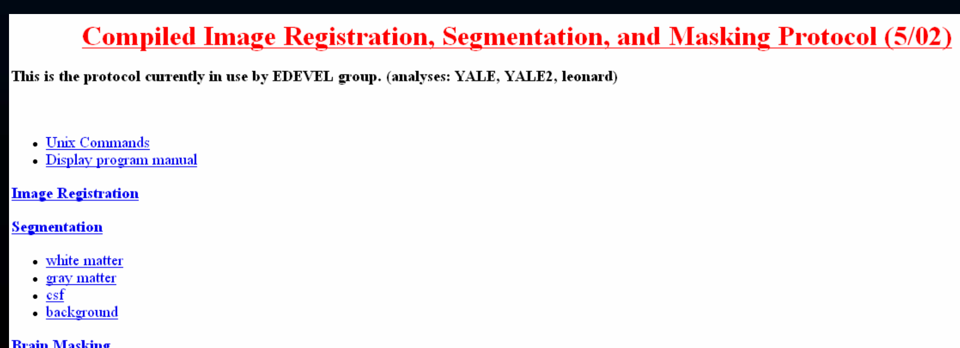


1. Large volume size for high resolution 3d MRI. (a typical size of 300x300x300)
2. Complex protocols for different cortical and sub-cortical structures.
3. Lack of efficient 3D tools for annotating the anatomical structures.
4. Hard to guarantee consistency among different neuroanatomists.
5. It is very time-consuming to fully delineate the brain anatomical structures even for a single volume. (It usually takes weeks or even months.)

Complex Protocols



http://www.loni.ucla.edu/~esowell/edevel/new_sulcvar.html



Compiled Image Registration, Segmentation, and Masking Protocol (5/02)

This is the protocol currently in use by EDEVEL group. (analyses: YALE, YALE2, leonard)

- Unix Commands
- Display program manual

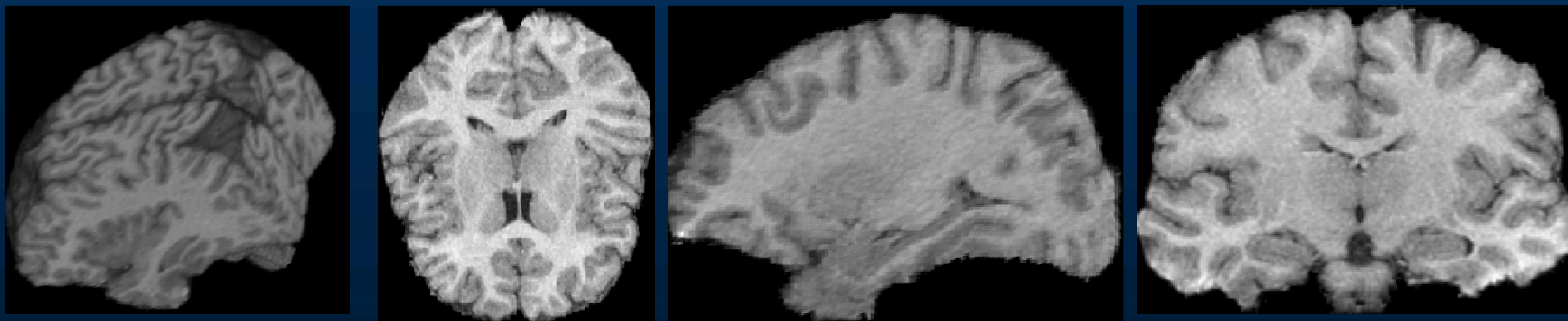
Image Registration

Segmentation

- white matter
- gray matter
- csf
- background

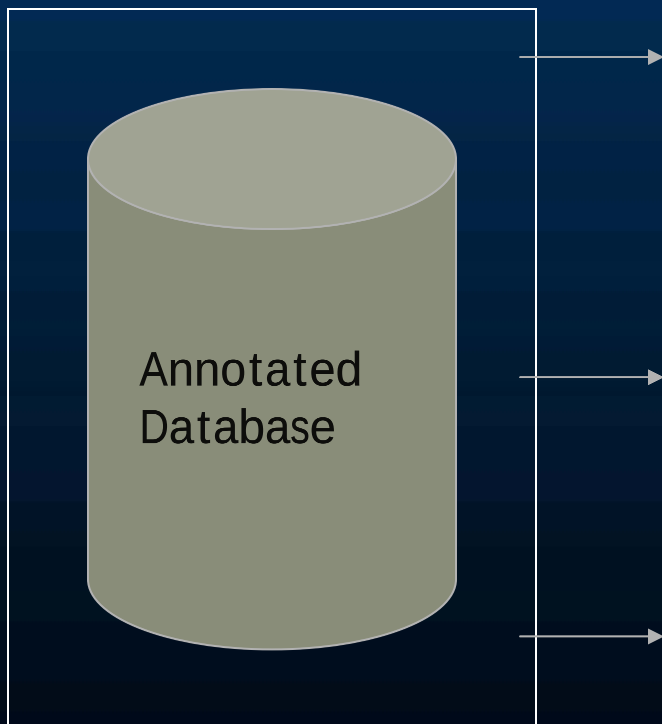
Brain Masking

Challenges for Automatic Segmentation



1. Large volume size for high resolution 3d MRI. (a typical size of 300x300x300)
2. Very weak intensity patterns. (large inter-class similarity and intra-class variation)
3. Hard to capture 3D shape info due to the high dimension space and limited number of training data.
4. Hard to capture the high-level knowledge and adapt to different protocols.

Framework



Learning based approaches to capture complex appearance models by integrating a large number of cues (intensity, curvatures, gradients)

Global shape prior.

A 3D representation to efficiently perform surface revolution.

To learn a hybrid discriminative/generative model to capture local and global shapes, and complex appearances.

A Learning Based Approach

- A learning based algorithm to perform efficient and effective brain structure parsing.
- The algorithm implicitly and explicitly combines hundreds of features to model complex objects.
- It is up to the learning procedure to learn protocols from examples, and is highly adaptive.
- Has nearly no parameters to tune.
- Explicit 3D representation can represent arbitrary number of regions and perform fast surface evolution.
- Has the potential to outperform human experts.

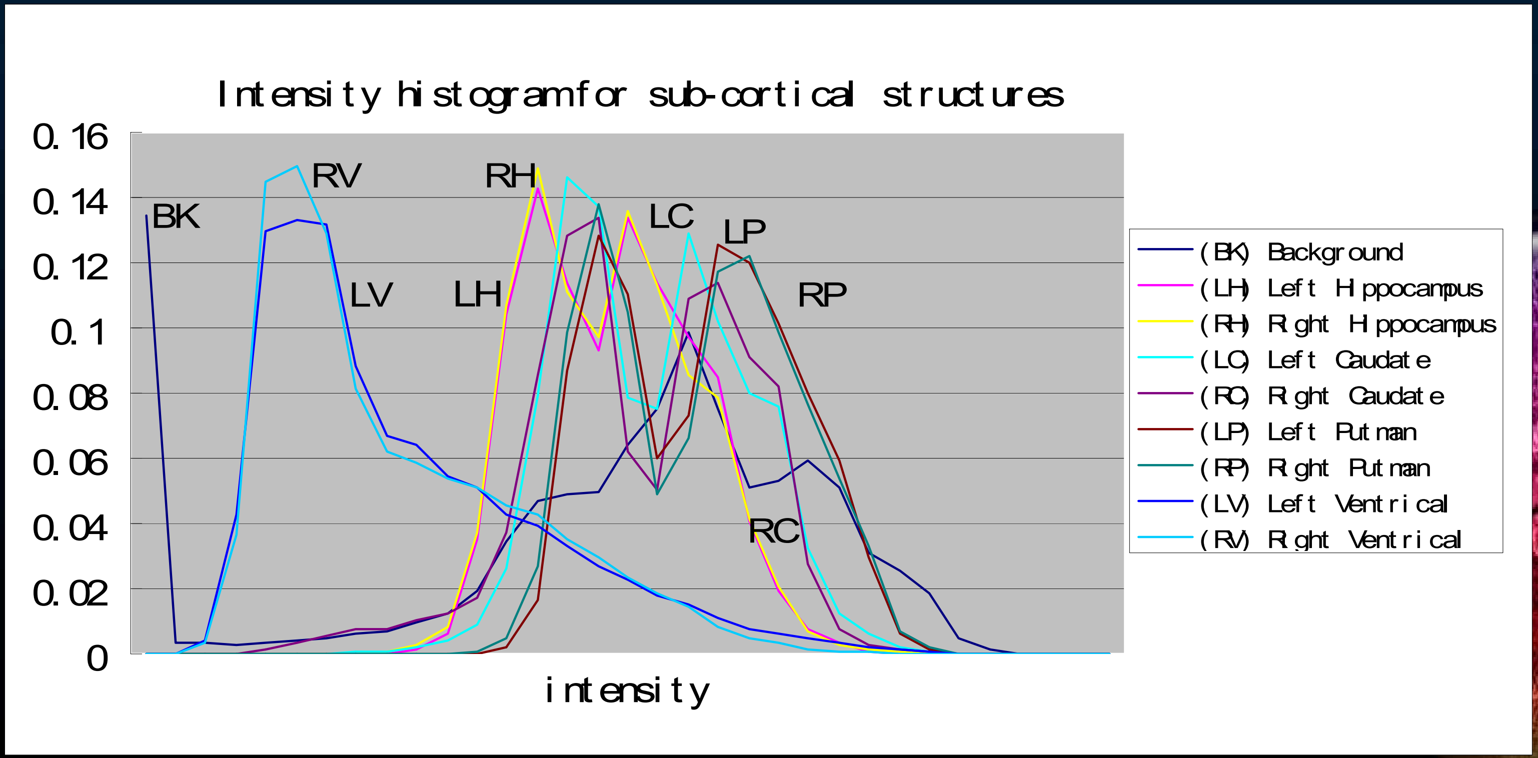
Bayesian Model

Input: V

Solution: $W = (R_1, R_2, \ldots, R_n)$

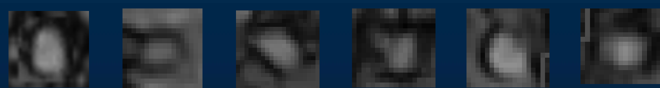
$$p(W \mid V) \propto p(V \mid W)\ p(W)$$

It is very hard to learn and compute the likelihood p(V|W) and prior p(W).

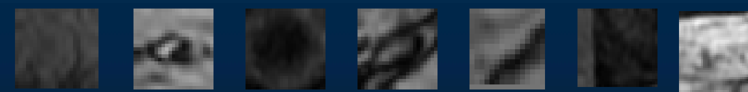


Discriminative v.s. Generative

For a data sample: x and its class label: $y \in \begin{cases} \{-1,+1\} & \textit{two class} \\ \{1,2,...,n\} & \textit{multi}-\textit{class} \end{cases}$



Positives, y=+1

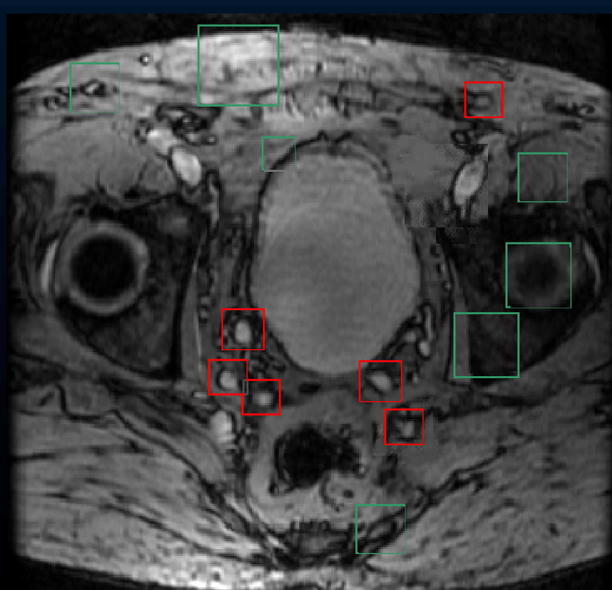


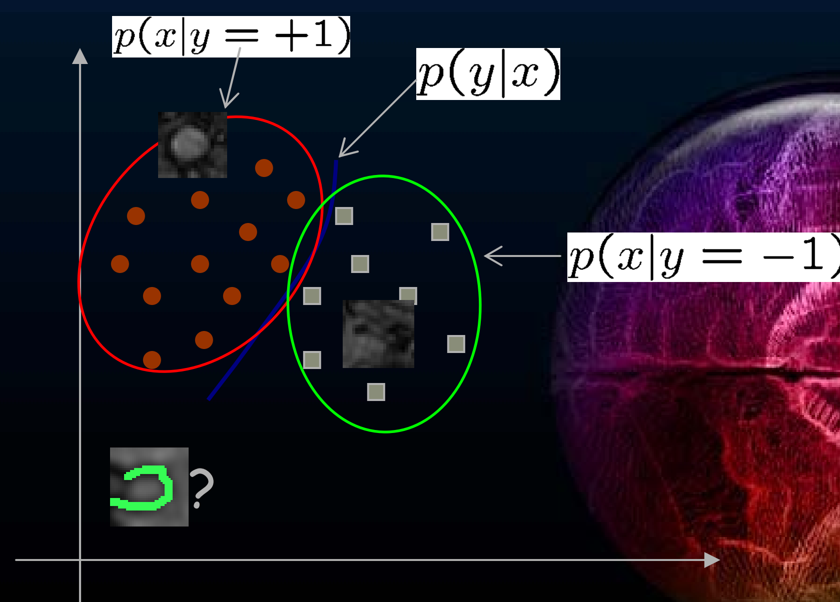
Negatives, y=-1

Discriminative model: $p(y|x)$

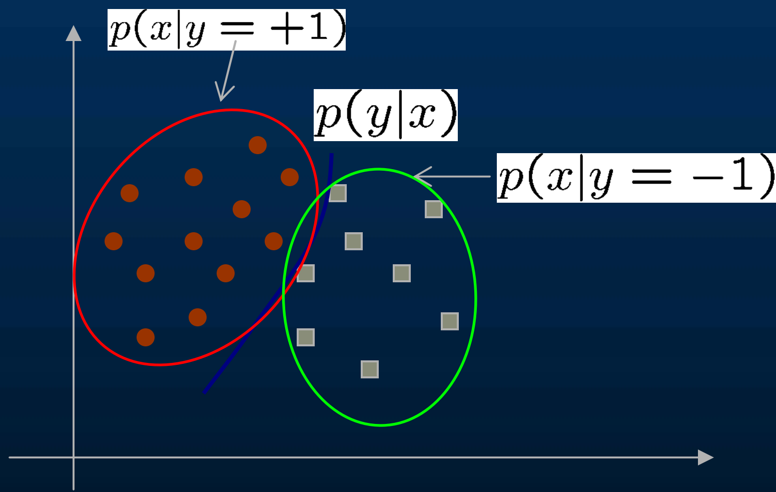
Generative model: $p(x|y),\ p(y)$

$$p(y|x) = \frac{p(x|y)p(y)}{\sum_y p(x|y)p(y)}$$



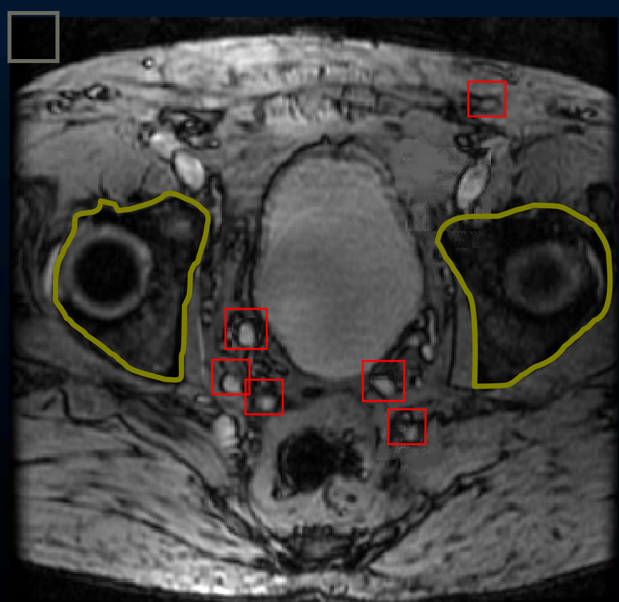


Discriminative v.s. Generative Models



$$p(y|x)$$

- Discriminative models are easier to learn/compute.
- They are focused on discrimination and marginal distributions.
- Its modeling power is limited since y is just a label.
- If you are asking, "Where are the lymph-nodes?", then you would probably want to use <u>discriminative methods</u>.



$$p(x|y),\ p(y)$$

- Generative models contains richer information.
- They are focused on single class.
- They explain the underlying generation process.
- If you are asking, "Find bone regions and describe their shapes.", then you would use <u>generative methods</u>.

Discriminative Models

$$E_1 = \alpha_1 \sum_{i=1}^{n} \sum_{s \in R_i} -\log p(l_s = i \,|\, V(N(s)))$$

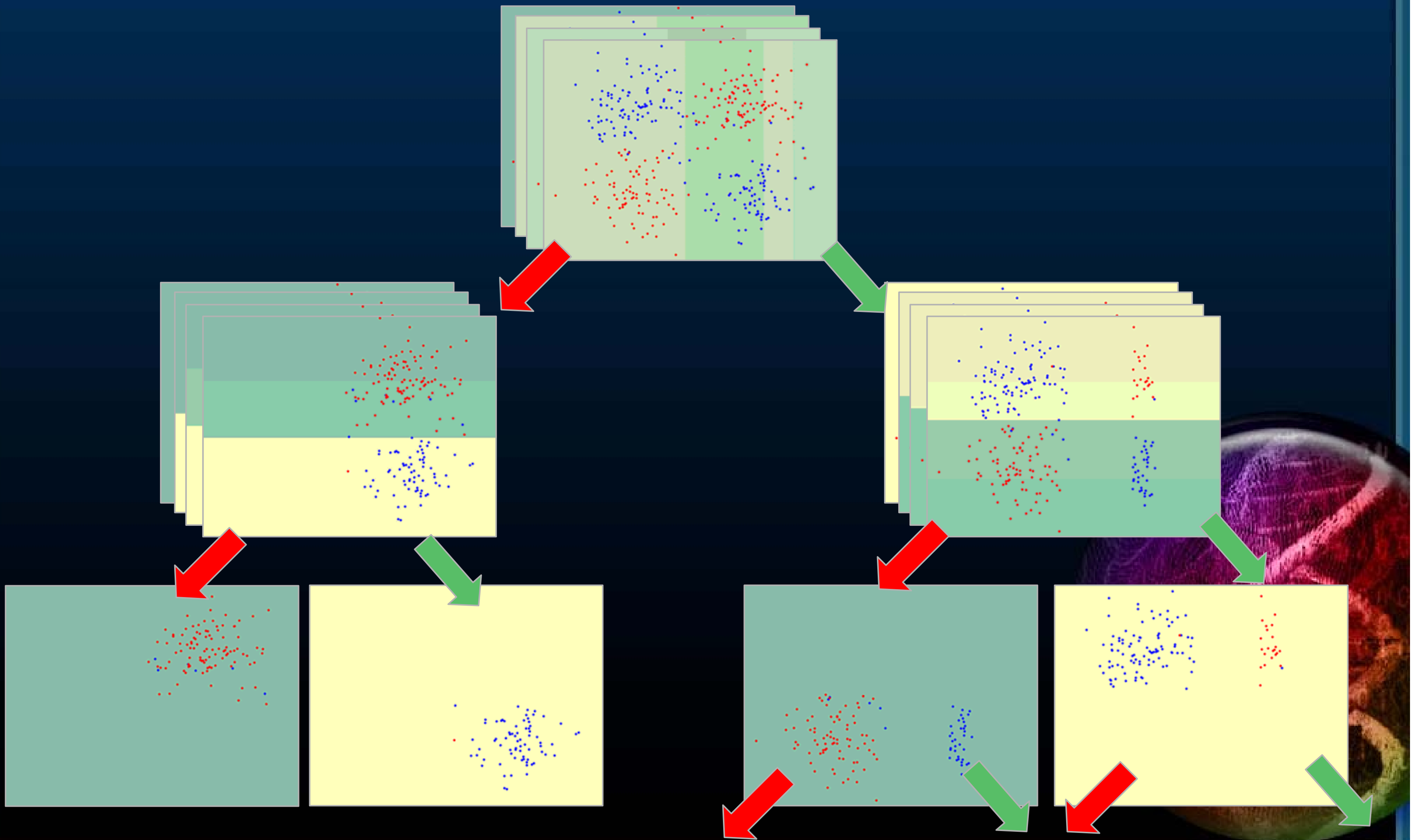
Discriminative (classification) model based on a local volume patch.

(1) It is capable of capturing complex appearance model based on a large context.

(2) Has much more representational power than i.i.d models.

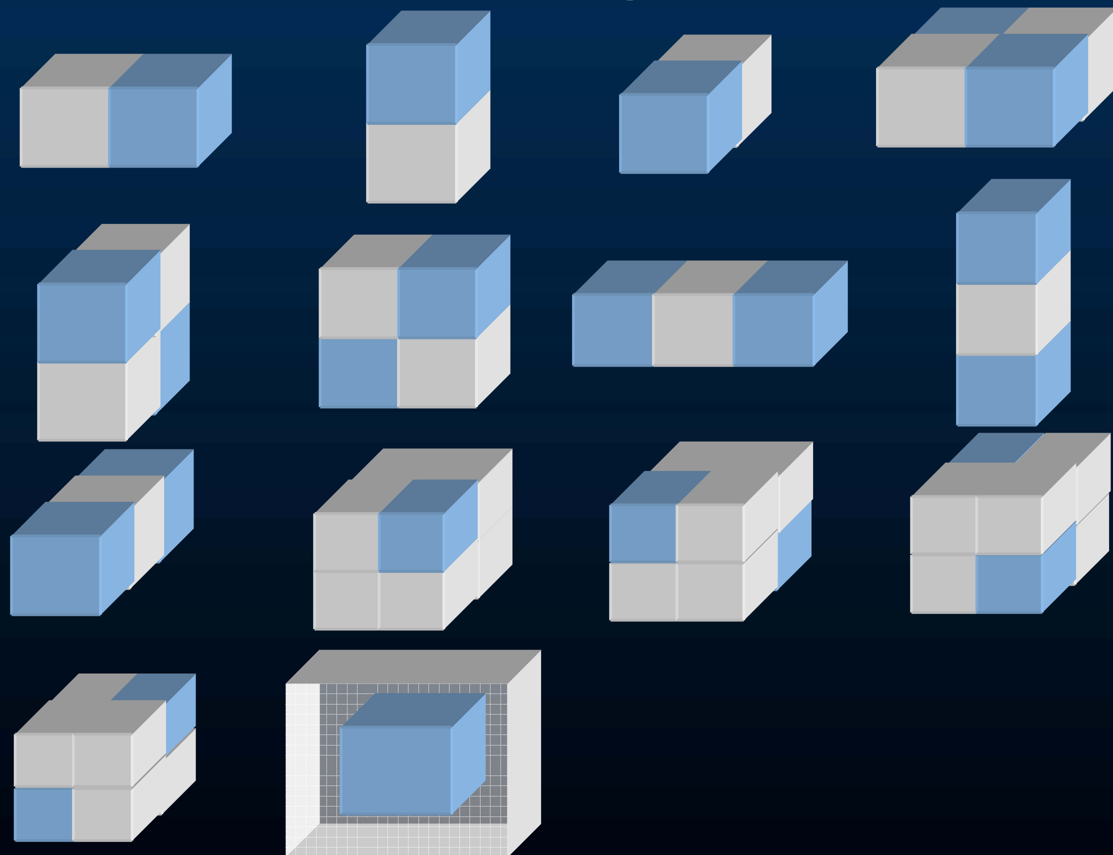
(3) Easy to learn and compute than a full generative model.

Probabilistic boosting trees (Z. Tu, ICCV 2005)



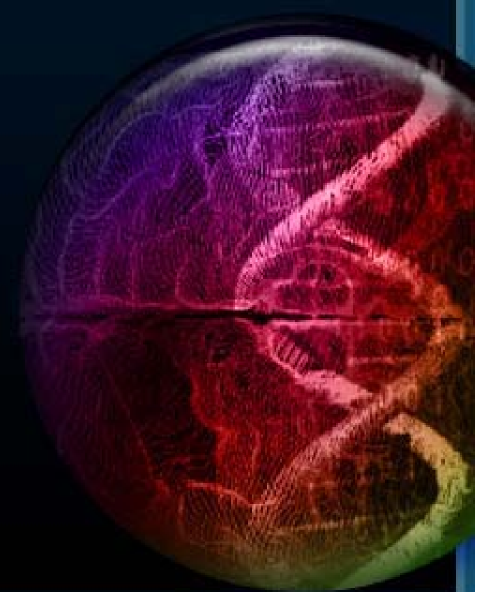
Features

Around 10,000 features in the candidate pool: Gradients, Curvatures, Haars

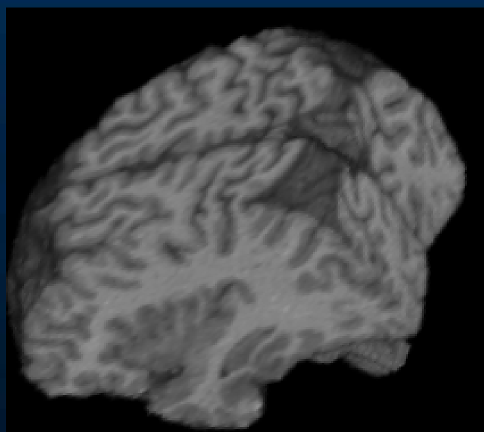


(1) Very fast to compute using integral volume.

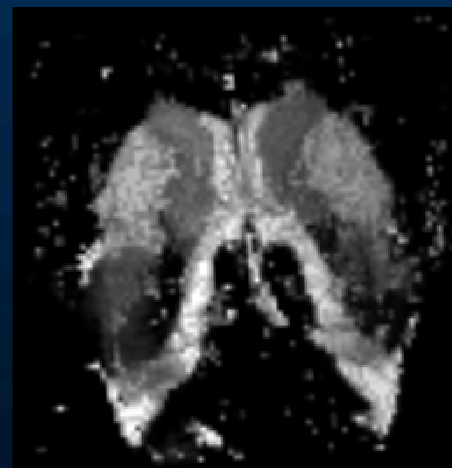
(2) Combine information at different scales.



Discriminative Models



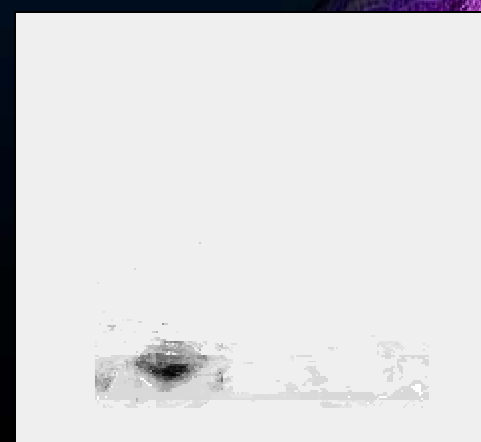
input



classification

$$p(l_s \,|\, V(N(s)))$$

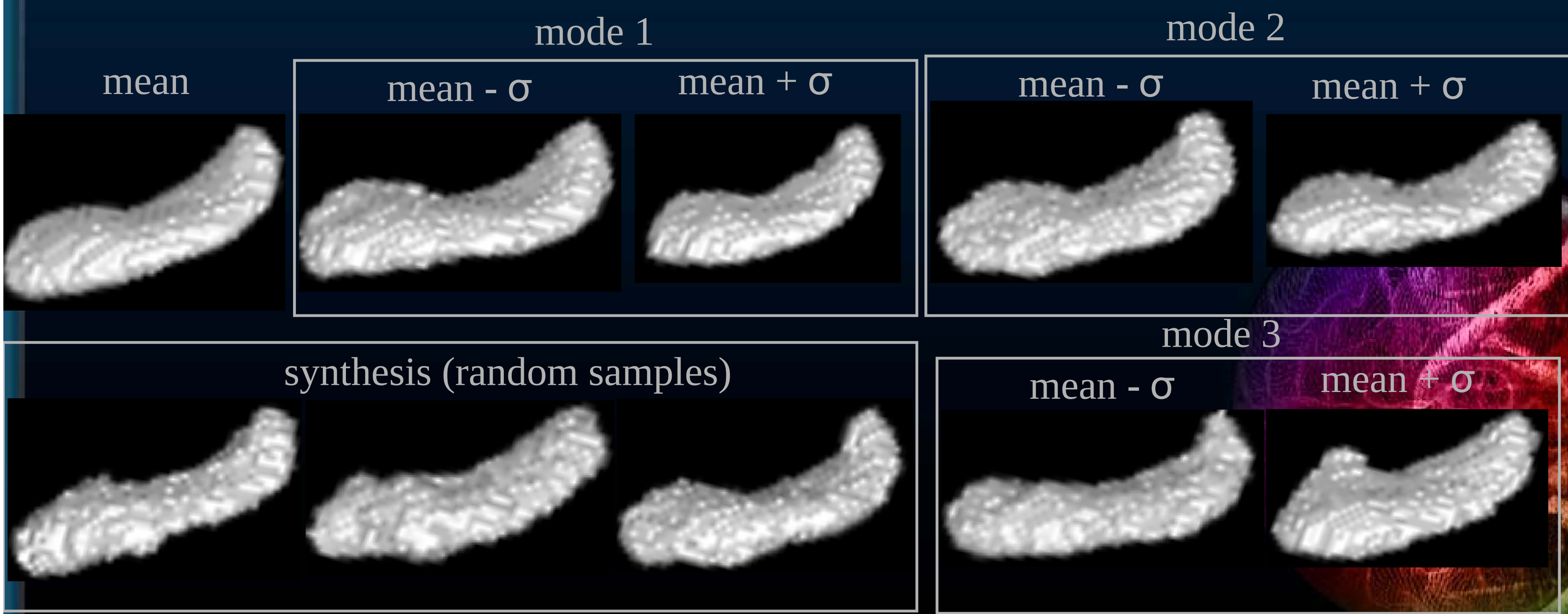
$$p(l_s = 1 \,|\, V(N(s)))$$



Shape PCA Priors

1. Building priors on 3D shapes is challenging.
2. Signed distance maps give an easy implementation.

$$S = U\alpha + \bar{S} \qquad Q = U\Sigma V^T$$



Hybrid Discriminative/Generative Models

$$\mathrm{E} = \alpha_1 \sum_{\mathrm{i}=1}^{\mathrm{n}} \sum_{\mathrm{s} \in \mathrm{R}_\mathrm{i}} -\log p(v_s, l_s = i \,|\, V(N/s)) +$$

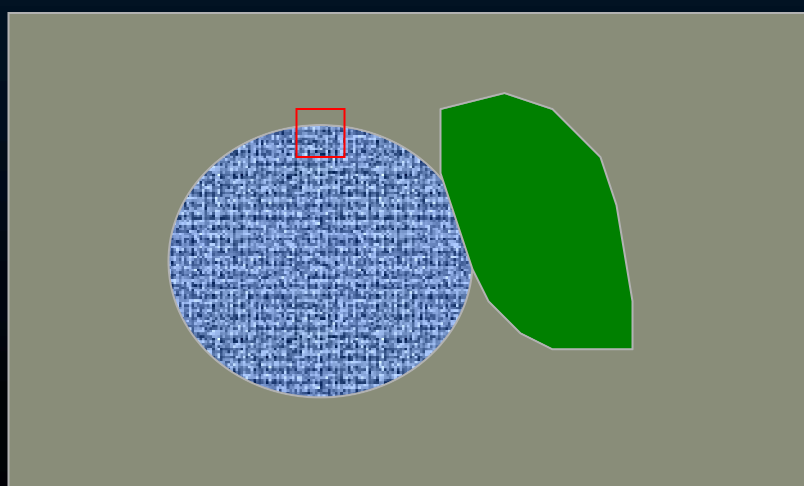
pseudo-likelihood
appearance model

$$\alpha_2 \sum_{i=2}^{n} -\log p_{PCA}(S_i) +$$

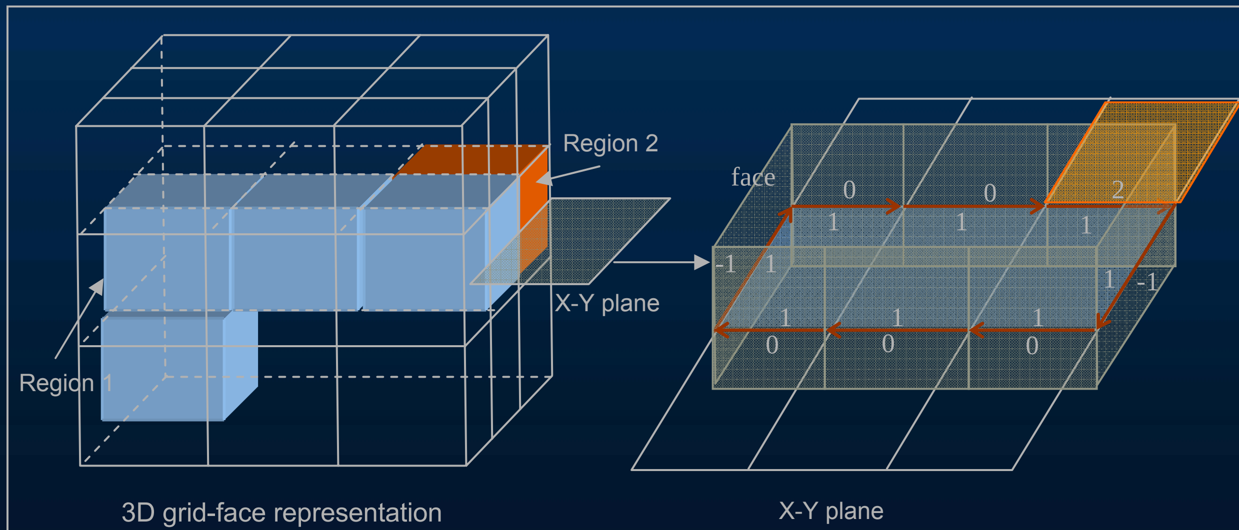
global shape prior

$$\alpha_3 \sum_{i=1}^{n} -\Lambda(S_i)$$

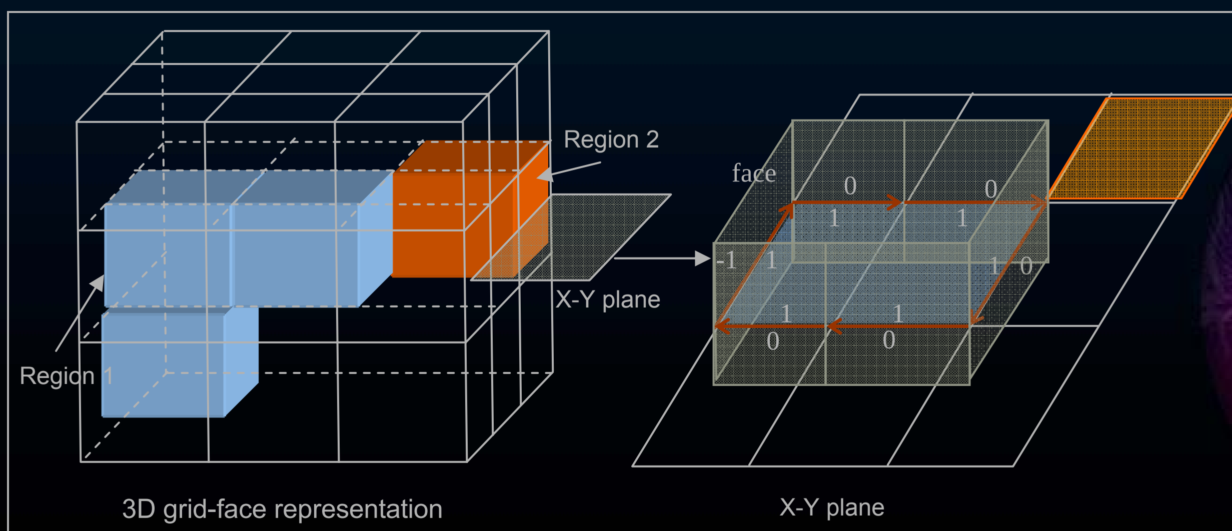
local smoothness prior



3D Representation



Surface
Evolution



The Algorithm

Training (given a set of annotated volumes):

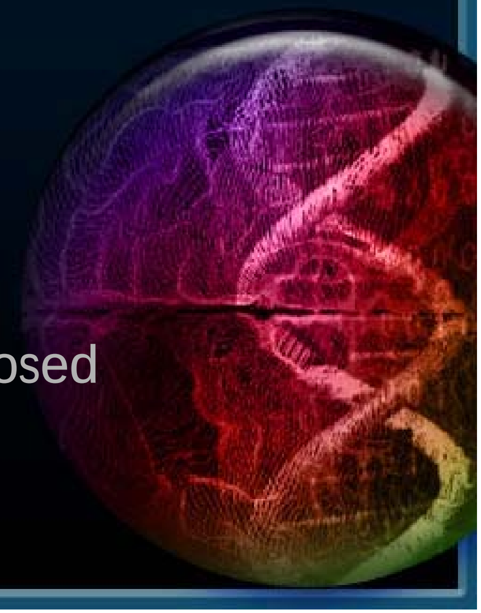
(1) Learn multi-class classification model using PBT.

(2) Learn PCA shape model for each structure.

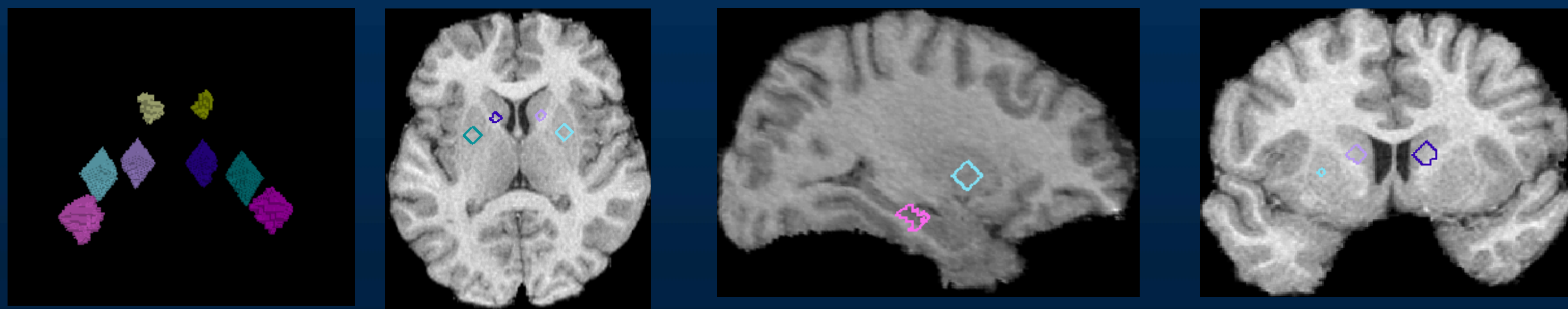
$$E = \alpha_1 \sum_{i=1}^{n} \sum_{s \in R_i} -\log p(l_s = i \mid V(N(s)) + \alpha_2 \sum_{i=2} -\log p(S_i) + \alpha_3 \sum_{i=1} -\Lambda(S_i)$$

Testing (given a volume)

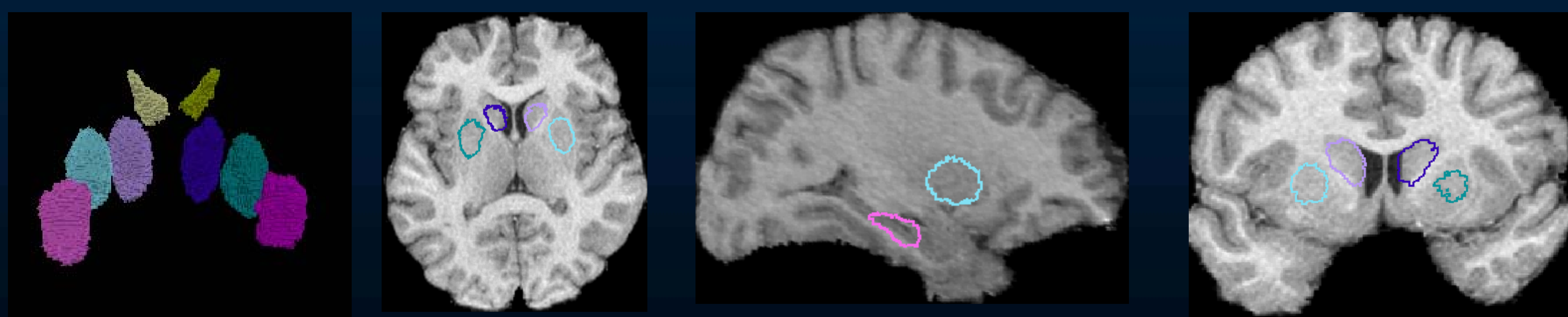
1. Compute classification using learned PBT.
2. Obtain the initial segmentation.
3. Perform region competition based on the proposed 3D representation.



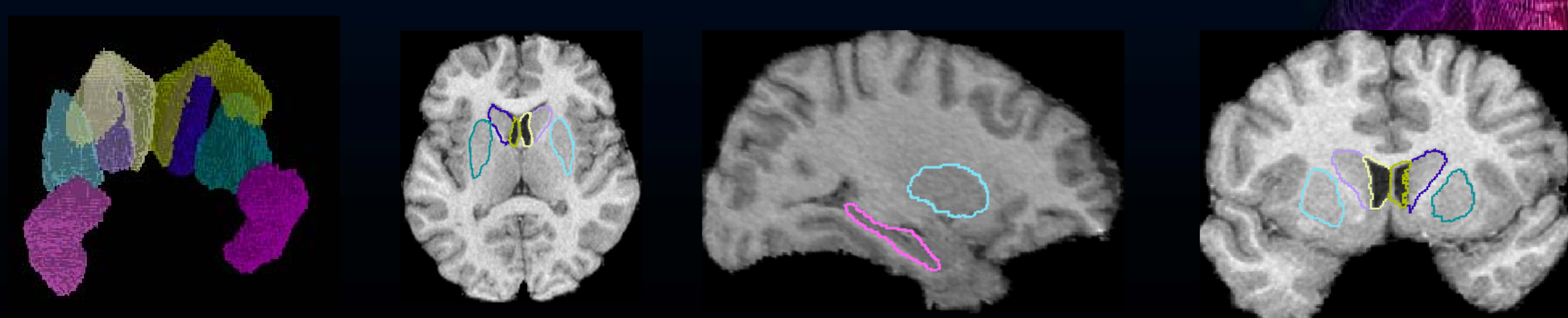
Results



Step=1

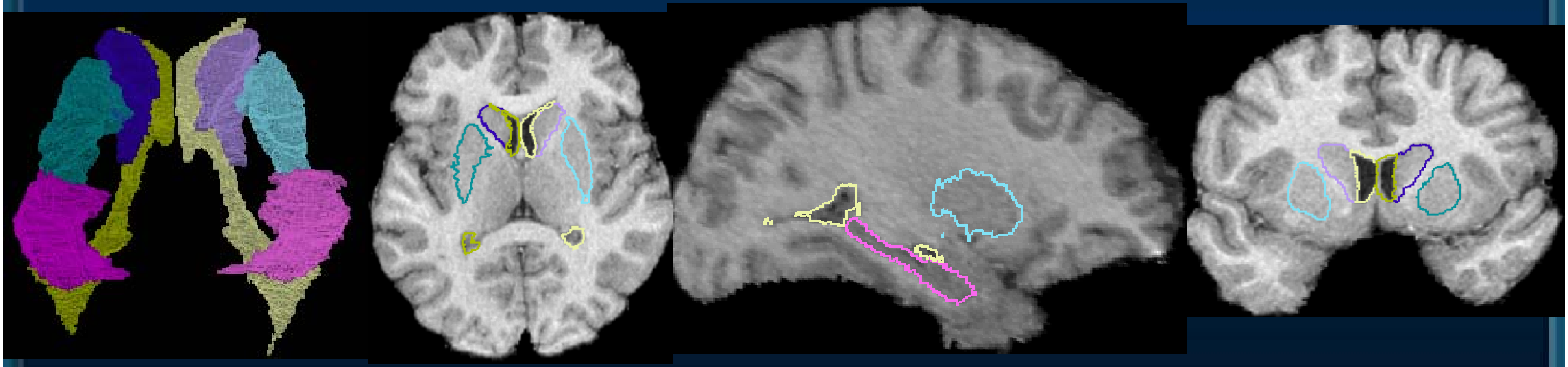


Step=2

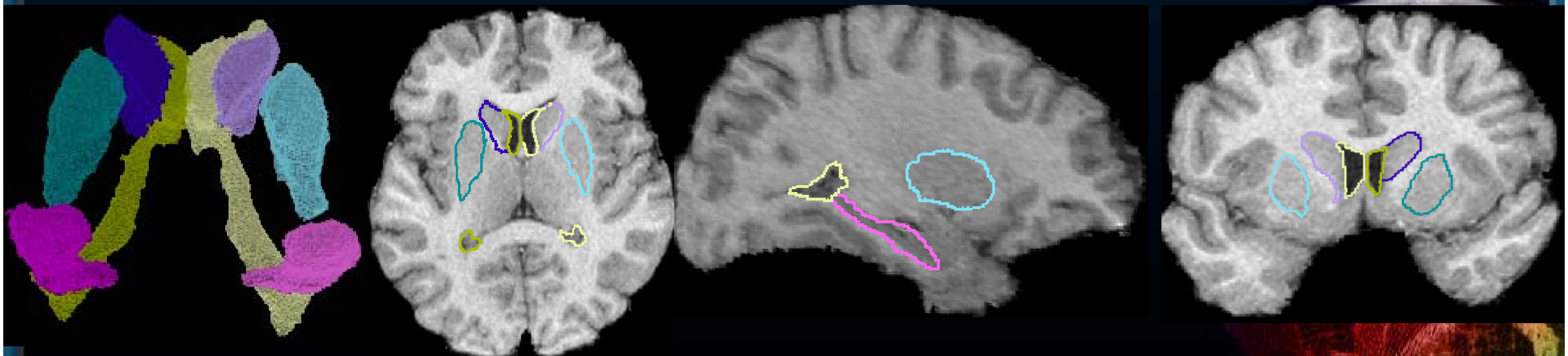


Step=2

Results on The Training Data

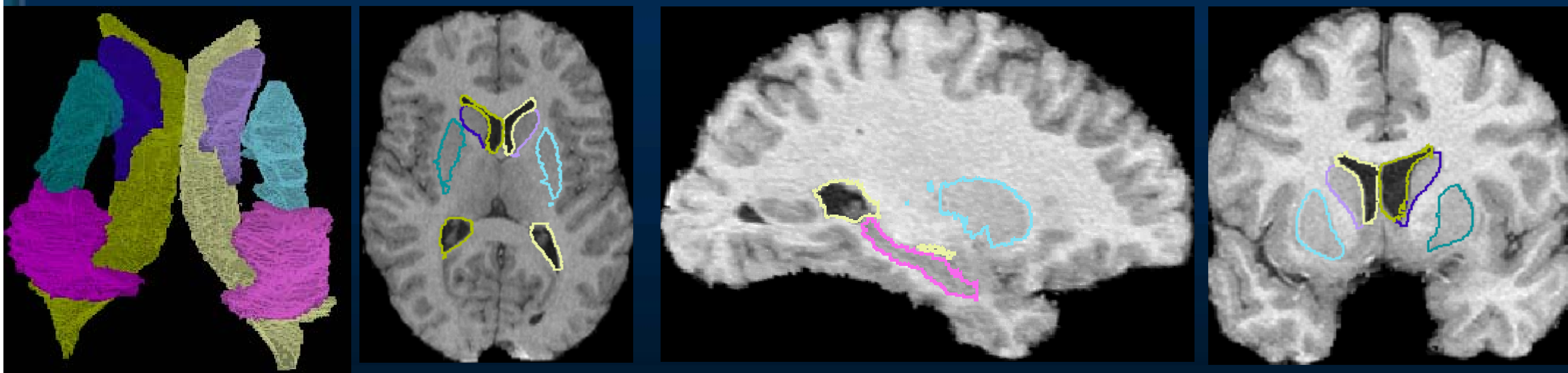


Manual annotation

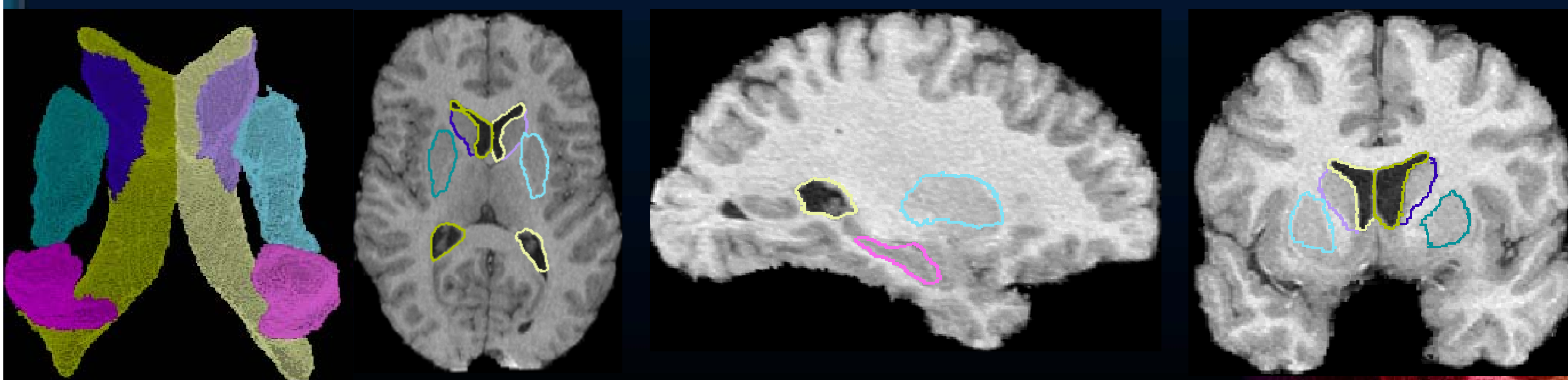


Automatic segmentation

Results on The Training Data

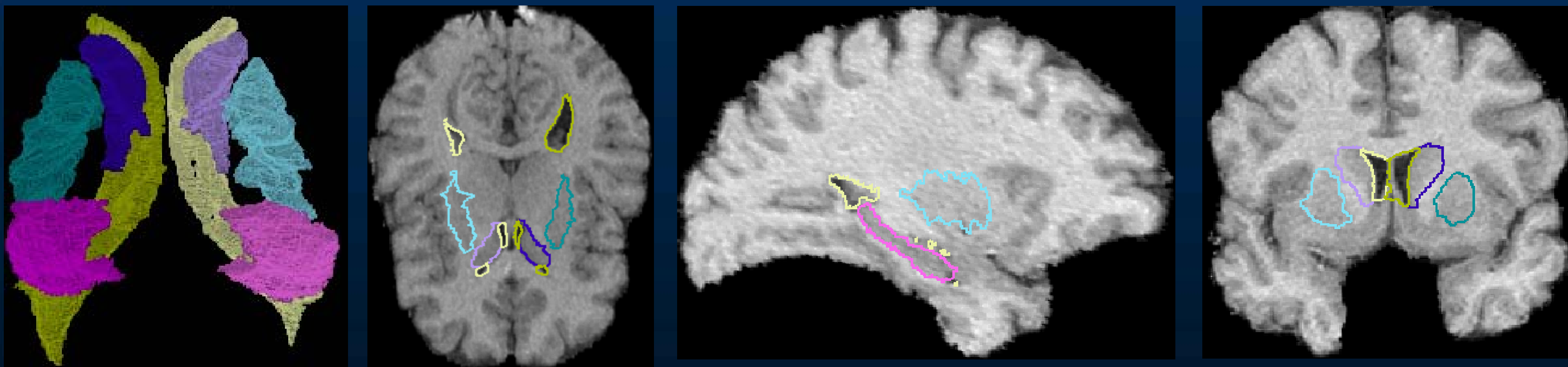


Manual annotation

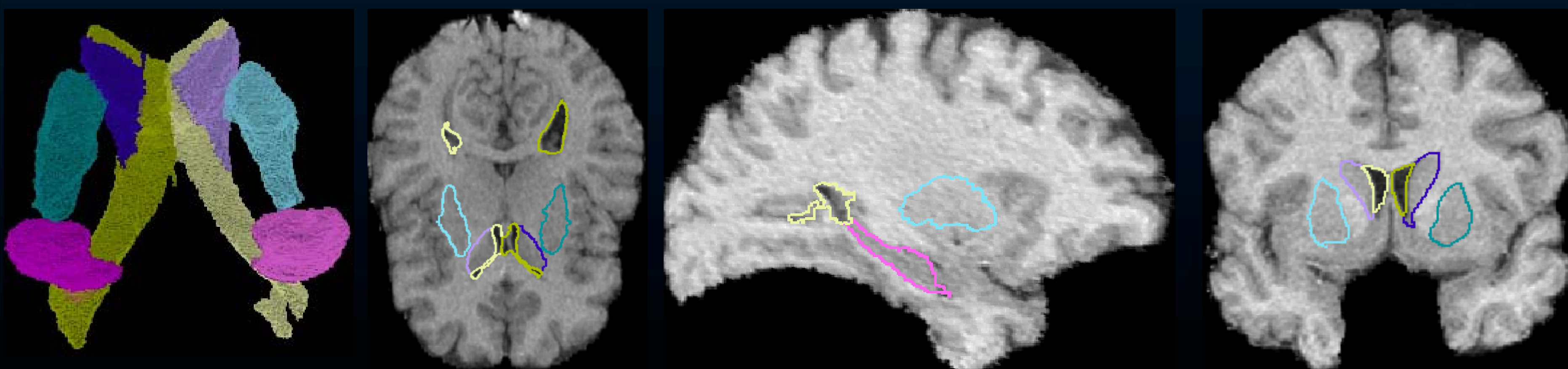


Automatic segmentation

Results on The Testing Data

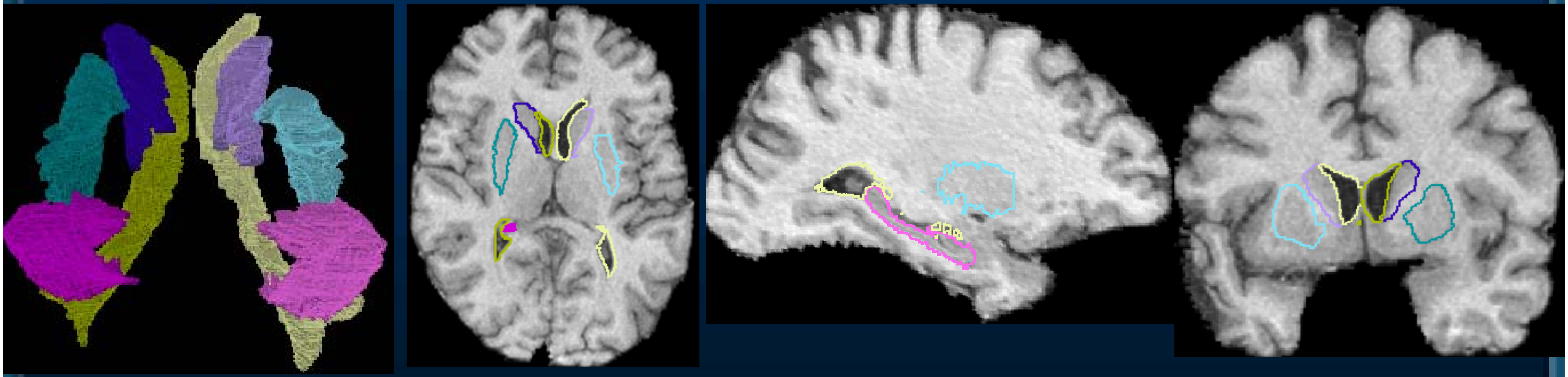


Manual annotation

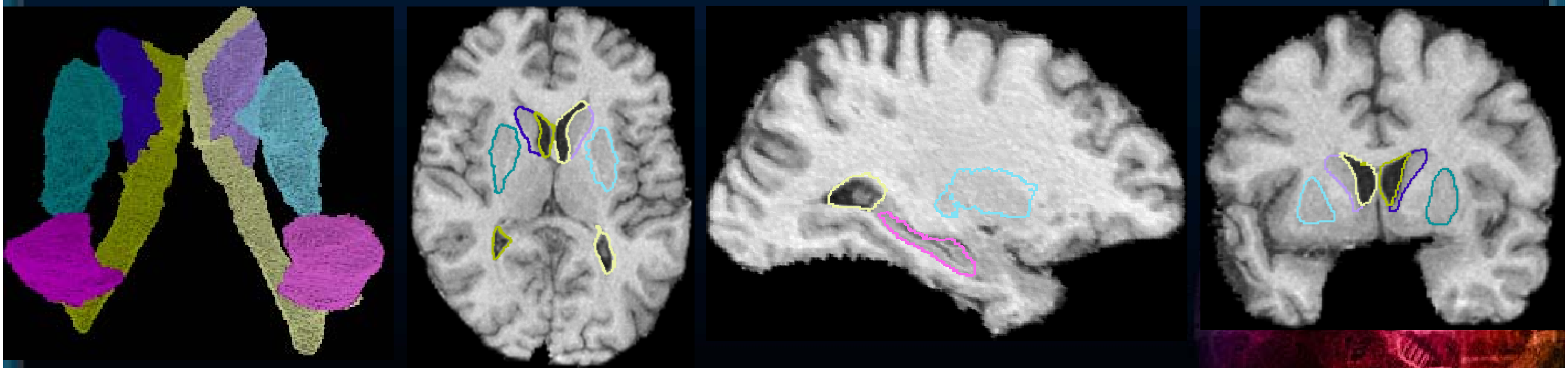


Automatic segmentation

Results on The Testing Data



Manual annotation



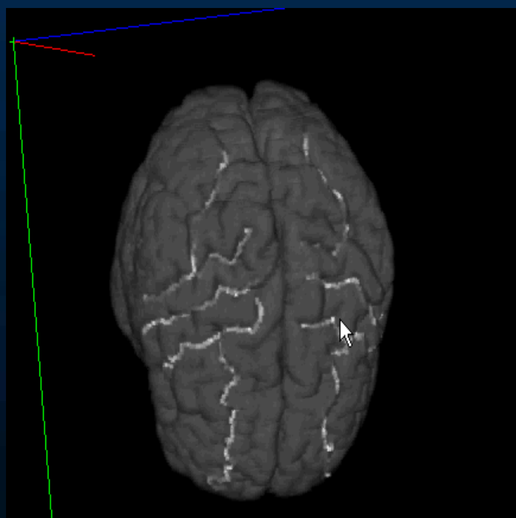
Automatic segmentation

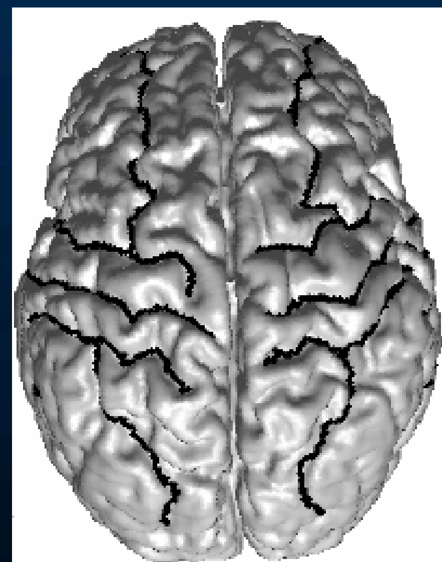
Evaluation

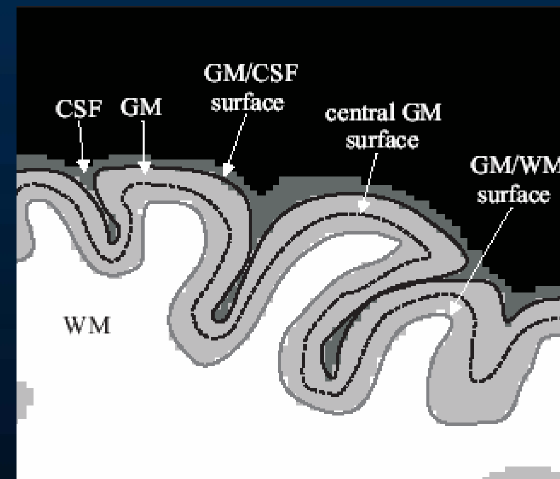
training	precision	recall	Hausdorff distances		mean	variance
Left Hippocampus	0.694	0.779	6.638	10.384	1.872	0.532
Right Hippocampus	0.675	0.715	9.975	11.863	2.213	0.517
Left Caudate	0.856	0.853	6.610	7.899	1.303	0.244
Right Caudate	0.835	0.849	4.988	8.606	1.332	0.361
Left Puteman	0.785	0.701	10.441	10.343	2.474	0.780
Right Puteman	0.779	0.781	8.552	9.673	2.006	0.390
Left Ventricle	0.914	0.817	5.592	16.007	1.117	0.386
Right Ventricle	0.910	0.815	6.022	13.915	0.994	0.131

testing	precision	recall	Hausdorff distances		mean	variance
Left Hippocampus	0.686	0.766	6.729	12.082	2.039	0.365
Right Hippocampus	0.620	0.644	14.284	13.576	2.835	1.105
Left Caudate	0.842	0.806	7.961	8.123	1.463	0.327
Right Caudate	0.811	0.825	6.694	8.525	1.443	0.290
Left Puteman	0.746	0.682	10.155	10.594	2.606	0.832
Right Puteman	0.751	0.721	10.079	9.443	2.377	0.762
Left Ventricle	0.904	0.808	6.345	11.432	1.102	0.260
Right Ventricle	0.897	0.813	6.904	14.675	1.097	0.239

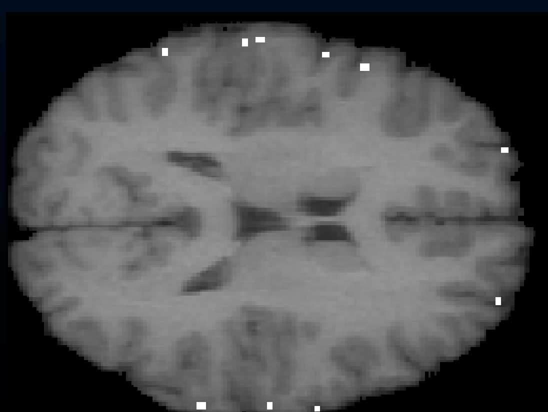
Automatic Sulci Detection

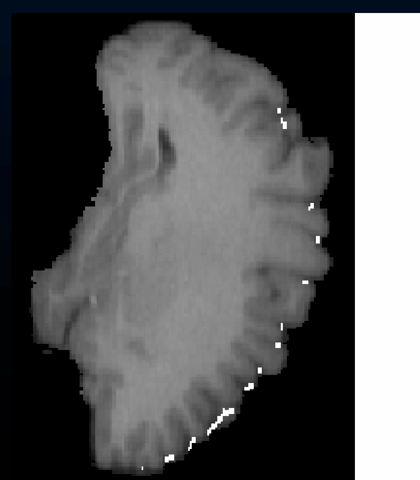




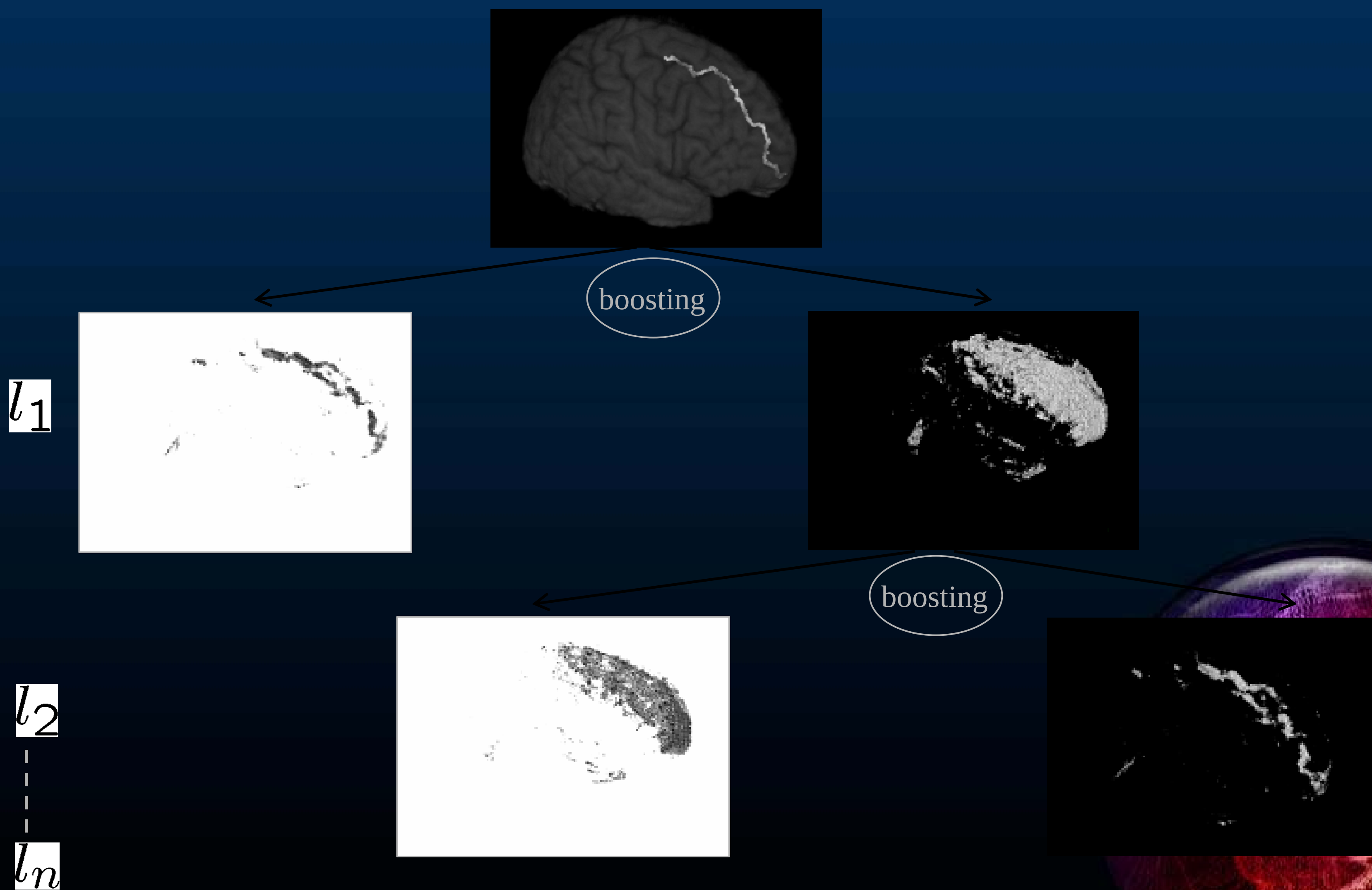


Tosun, et al. 2005



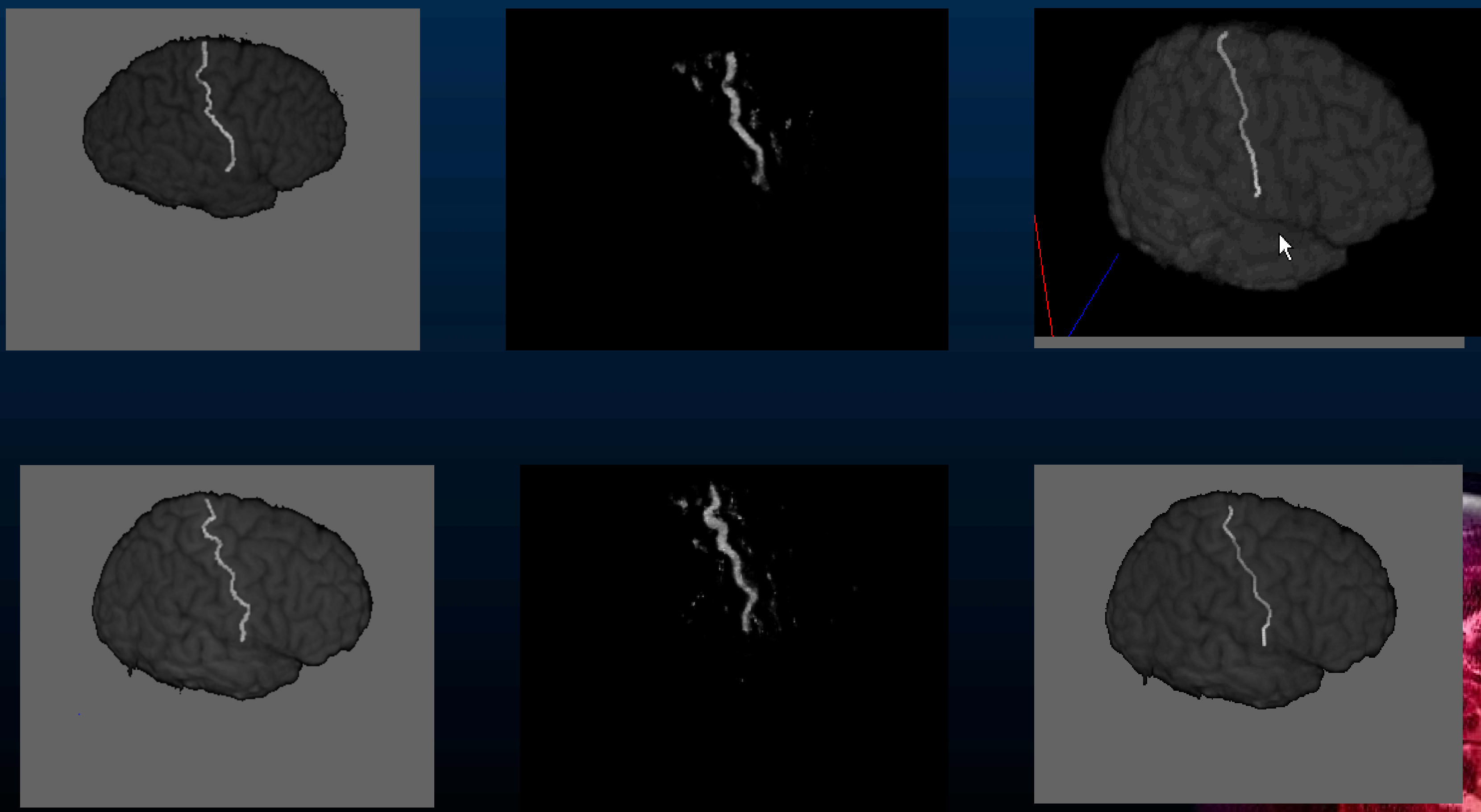


PBT



Results

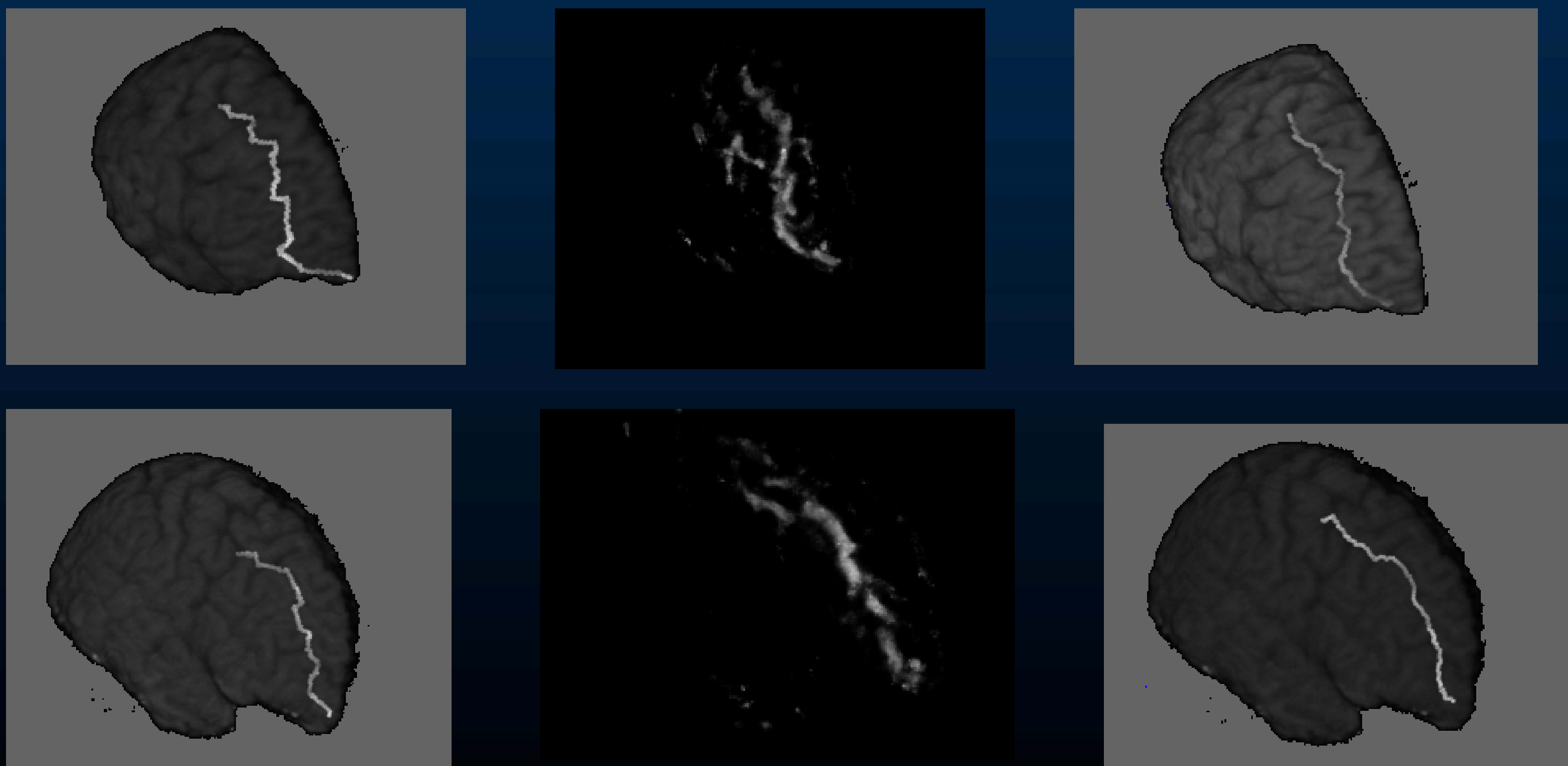
True | Prob | Result



Results on Training set: Central sulcus

Results

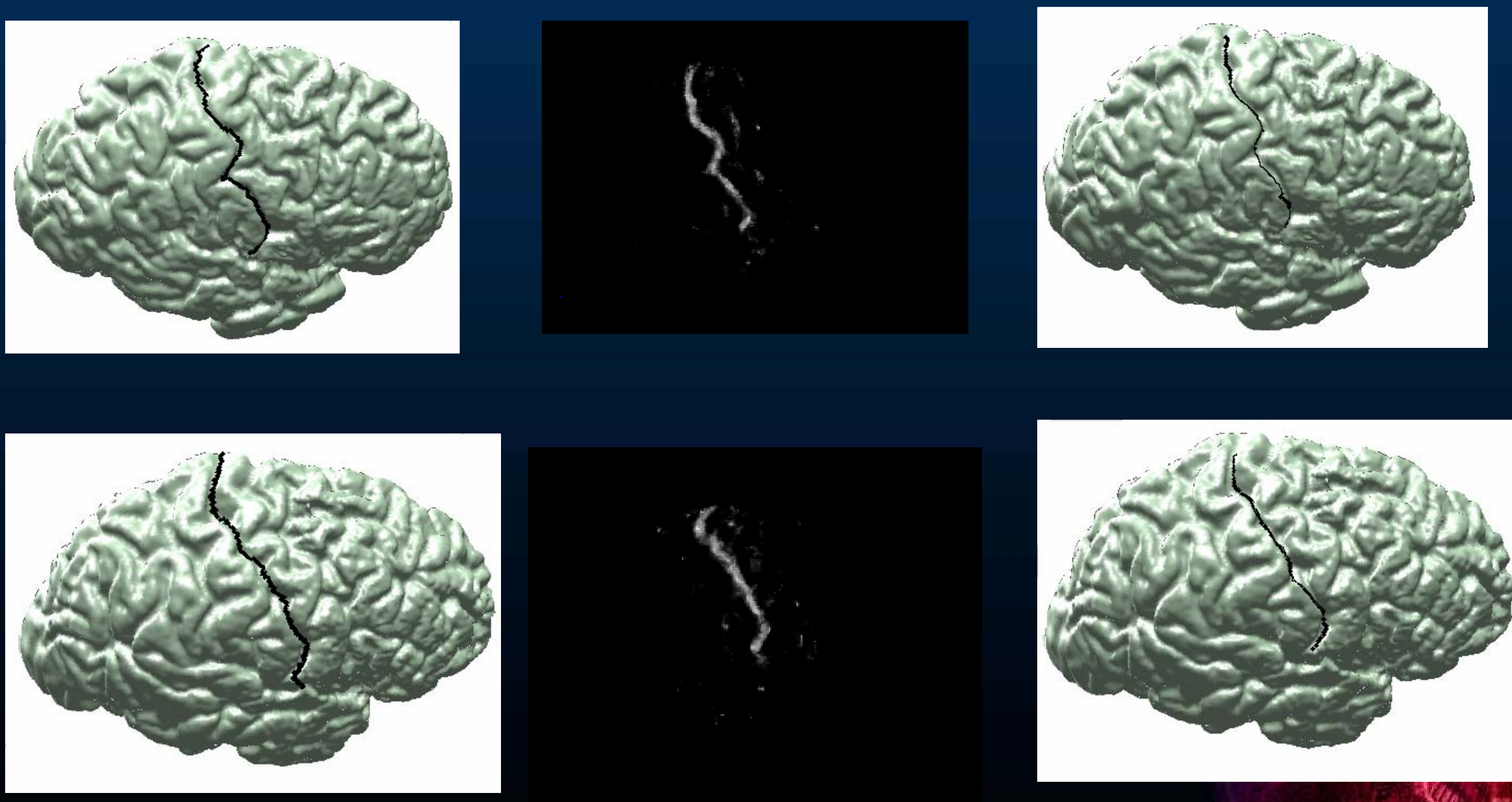
True | Prob | Result



Results on Testing set: Superior Frontal sulcus

Results on Surfaces

True | Prob | Result



Results on Training set: central sulci on surface

Evaluation

$$H(C,G) = \max_{c \in C} \min_{g \in G} \|c - g\|, \quad H_{av}(C,G) = \frac{1}{|C|} \sum_{c \in C} \min_{g \in G} \|c - g\|$$

Dataset	$< H_{av}(C_i, G_i) >$	$< H_{av}(G, C) >$	$< H_{wor}(C, G) >$
Testing (Central on MRI)	2.7374	3.4614	7.5356
Central (Central on MRI)	3.7643	4.2176	8.5567
Testing (Superior Frontal on MRI)	4.2634	4.5982	12.0444
Training (Superior Frontal on MRI)	4.0973	4.4664	8.9999
Testing (Central on surface)	2.7937	3.0723	9.4791
Training (Central on surface)	2.4393	2.8869	8.4413

1. It is a general framework and it works either on MRI volumes or extracted surfaces.
2. There is nearly no parameter to tune and learns the discriminative models from examples.
3. Does not need to specify which major cortical sulcus.
4. No segmentation is needed, nor the process of mapping to a canonical view.
5. The algorithm is robust and fast.